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SEQUENCE LISTING

<110> Chambon, Pierre - Metzger, Daniel

<120> Transgenic mouse for targeted recombination mediated by modified Cre-ER

<130> D18961

<150> FR 00 12 570

<151> 2000-10-03

<160> 14

<170> PatentIn Ver. 2.1

<210> 1

<211> 1788

<212> DNA

<213> Homo sapiens

 $\langle 220 \rangle$

<221> CDS

<222> (1) . . (1788)

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Gln Ile Gln Gly Asn Glu Leu Glu Pro Leu Asn Arg Pro Gln Leu Lys
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atc ccc ctg gag cgg ccc ctg ggc gag gtg tac ctg gac agc agc aag 144
Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
35 40 45

ccc gcc gtg tac aac tac ccc gag ggc gcc gcc tac gag ttc aac gcc 192
Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
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gcg gcc gcc gcc aac gcg cag gtc tac ggt cag acc ggc ctc ccc tac 240
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ggc ccc ggg tct gag gct gcg gcg ttc ggc tcc aac ggc ctg ggg ggt 288
Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
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ttc ccc cca ctc aac agc gtg tct ccg agc ccg ctg atg cta ctg cac 336
 Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
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ccg ccg ccg cag ctg tgc cct ttc ctg cag ccc cac ggc cag cag gtg 304
Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
115 120 125

ccc tac tac ctg gag aac gag ccc agc ggc tac acg gtg cgc gag gcc 432
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 Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
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gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat gct 576
 Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
 180 185 190

tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc ttc 624
 Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
 195 200 205

ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc acc 672
 Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
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aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc tgc 720
 Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
 225 230 235 240

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 Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
 245 250 255

aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga gat 816
 Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
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gat ggg gag ggc agg ggt gaa gtg ggg tct gct gga gac atg aga gct 864
 Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
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agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg ttg 960
 Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
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gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga ccc 1008
 Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
 325 330 335

ttc agt gaa gct tcg atg atg ggc tta ctg acc aac ctg gca gac agg 1056
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
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 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
 405 410 415
 tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca tca 1296
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
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 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
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 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
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 acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg gac 1440
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
 aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg acc 1488
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 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
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 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
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 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
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 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
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 Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser Ser
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 cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc cct 1776
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 <212> PRT
 <213> Homo sapiens

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Ile Pro Leu Glu Arg Pro Leu Gly Glu Val Tyr Leu Asp Ser Ser Lys
 35 40 45

Pro Ala Val Tyr Asn Tyr Pro Glu Gly Ala Ala Tyr Glu Phe Asn Ala
 50 55 60

Ala Ala Ala Ala Asn Ala Gln Val Tyr Gly Gln Thr Gly Leu Pro Tyr
 65 70 75 80

Gly Pro Gly Ser Glu Ala Ala Ala Phe Gly Ser Asn Gly Leu Gly Gly
 85 90 95

Phe Pro Pro Leu Asn Ser Val Ser Pro Ser Pro Leu Met Leu Leu His
 100 105 110

Pro Pro Pro Gln Leu Ser Pro Phe Leu Gln Pro His Gly Gln Gln Val
 115 120 125

Pro Tyr Tyr Leu Glu Asn Glu Pro Ser Gly Tyr Thr Val Arg Glu Ala
 130 135 140

Gly Pro Pro Ala Phe Tyr Arg Pro Asn Ser Asp Asn Arg Arg Gln Gly
 145 150 155 160

Gly Arg Glu Arg Leu Ala Ser Thr Asn Asp Lys Gly Ser Met Ala Met
 165 170 175

Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr Ala
 180 185 190

Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala Phe
 195 200 205

Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala Thr
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Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala Cys
 225 230 235 240

Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile Arg
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Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg Asp
 260 265 270

Asp Gly Glu Gly Arg Gly Glu Val Gly Ser Ala Gly Asp Met Arg Ala
 275 280 285

Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys Asn
 290 295 300

Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu Leu
 305 310 315 320

Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg Pro
 325 330 335
 Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp Arg
 340 345 350
 Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe Val
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 Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp Leu
 370 375 380
 Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro Gly
 385 390 395 400
 Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly Lys
 405 410 415
 Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr Ser
 420 425 430
 Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys Leu
 435 440 445
 Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser Ser
 450 455 460
 Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu Asp
 465 470 475 480
 Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu Thr
 485 490 495
 Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu Ser
 500 505 510
 His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser Met
 515 520 525
 Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met Leu
 530 535 540
 Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser Val
 545 550 555 560
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 Ala Thr Val
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<210> 3
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 <212> DNA
 <213> Artificial sequence

<220>

<221> CDS

<222> (1)..(1983)

<220>

<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg	
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gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt	144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val	
35 40 45	
tgc cgg tgc tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt	192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe	
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ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg	240
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala	
65 70 75 80	
cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac	288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn	
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atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct	336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala	
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gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt	384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
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145 150 155 160	
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu	
165 170 175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	
195 200 205	
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672

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Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
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tac	ggc	gct	aag	gat	gac	tct	ggt	cag	aga	tac	ctg	gcc	tgg	tct	gga	864
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
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His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
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tca	ata	ccg	gag	atc	atg	caa	gct	ggt	ggc	tgg	acc	aat	gta	aat	att	960
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Tyr	Thr	Asn	Val	Asn	Ile	
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Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
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cgc	ctg	ctg	gaa	gat	ggc	gat	ctc	gag	cca	tct	gct	gga	gac	atg	aga	1056
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
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gct	gcc	aac	ctt	tgg	cca	agc	ccg	ctc	atg	atc	aaa	cgc	tct	aag	aag	1104
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
		355					360					365				
aac	agc	ctg	gcc	ttg	tcc	ctg	acg	gcc	gac	cag	atg	gtc	agt	gcc	ttg	1152
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
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Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385					390					395					400	
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Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
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agg	gag	ctg	gtt	cac	atg	atc	aac	tgg	gcg	aag	agg					

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agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Lys Asp His Ile His Arg Val Leu 530 535 540			1632
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acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575			1728
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ctg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 610 615 620			1872
gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser 625 630 635 640			1920
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<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

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 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
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Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205

Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220

Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240

Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
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Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270

Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285

His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300

Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
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Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
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Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
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Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
355 360 365

Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
370 375 380

Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
385 390 395 400

Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
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Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
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Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
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Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
450 455 460

Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
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Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
485 490 495

Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
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Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
515 520 525

Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu
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Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
545 550 555 560

Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
565 570 575

Ser His Ile Arg His Met Ser Asn Lys Arg Met Glu His Leu Tyr Ser
580 585 590

Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Met
595 600 605

Leu Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
610 615 620

Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
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<210> 5
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<212> DNA
<213> Artificial sequence

<220>
<221> CDS
<222> (1)..(1983)

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<223> Chimeric sequence Homosapiens-Bacteriophage P1

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gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96
Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
20 25 30
gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45
tgc cgg tgc tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
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ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80
cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95
atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110
gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag 432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat 480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa 528

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Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175
 att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga 576
 Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190
 atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt 624
 Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
 195 200 205
 gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg 672
 Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
 210 215 220
 att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc 720
 Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
 225 230 235 240
 cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta 768
 Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
 245 250 255
 tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att 816
 Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270
 tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga 864
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285
 cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt 912
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300
 tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att 960
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320
 gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg 1008
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335
 cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga 1056
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350
 gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag 1104
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365
 aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg 1152
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380
 ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga 1200
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400
 ccc ttc agt gaa gct tcg atg atg gcc tta ctg acc aac ctg gca gac 1248
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp

405	410	415	
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420 425 430			1296
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435 440 445			1344
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450 455 460			1392
gtg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 465 470 475 480			1440
aaa tgt gta gag ggc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 490 495			1488
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 500 505 510			1536
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515 520 525			1584
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530 535 540			1632
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 560			1680
acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575			1728
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580 585 590			1776
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala 595 600 605			1824
gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 610 615 620			1872
gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser 625 630 635 640			1920
tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe 645 650 655			1968

14

cct gcc aca gct tga
Pro Ala Thr Ala
660

1983

<210> 6
<211> 660
<212> PRT
<213> Artificial sequence
<223> Chimeric sequence Homosapiens-Bacteriophage P1

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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
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Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
35 40 45
Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
50 55 60
Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
65 70 75 80
Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
85 90 95
Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
100 105 110
Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
115 120 125
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
130 135 140
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
145 150 155 160
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
165 170 175
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
180 185 190
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly
195 200 205
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp
210 215 220
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys
225 230 235 240
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu
245 250 255

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Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile
 260 265 270
 Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly
 275 280 285
 His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val
 290 295 300
 Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile
 305 310 315 320
 Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val
 325 330 335
 Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg
 340 345 350
 Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys
 355 360 365
 Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu
 370 375 380
 Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg
 385 390 395 400
 Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp
 405 410 415
 Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe
 420 425 430
 Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp
 435 440 445
 Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro
 450 455 460
 Val Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly
 465 470 475 480
 Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr
 485 490 495
 Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys
 500 505 510
 Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser
 515 520 525
 Ser Thr Leu Lys Ser Leu Glu Lys Asp His Ile His Arg Val Leu
 530 535 540
 Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu
 545 550 555 560
 Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu
 565 570 575
 Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser

580 585 590
 Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala
 595 600 605
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655
 Pro Ala Thr Ala
 660

<210> 7
 <211> 1983
 <212> DNA
 <213> Artificial sequence

<220>
 <221> CDS
 <222> (1)..(1983)
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 <223> Chimeric sequence Homosapiens-Bacteriophage P1

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 Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
 1 5 10 15
 gat gca acg agt gat gag gtt cgc aag aac ctg atg gac atg ttc agg 96
 Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30
 gat cgc cag gcg ttt tct gag cat acc tgg aaa atg ctt ctg tcc gtt 144
 Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45
 tgc cgg tgg tgg gcg gca tgg tgc aag ttg aat aac cgg aaa tgg ttt 192
 Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60
 ccc gca gaa cct gaa gat gtt cgc gat tat ctt cta tat ctt cag gcg 240
 Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80
 cgc ggt ctg gca gta aaa act atc cag caa cat ttg ggc cag cta aac 288
 Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95
 atg ctt cat cgt cgg tcc ggg ctg cca cga cca agt gac agc aat gct 336
 Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110
 gtt tca ctg gtt atg cgg cgg atc cga aaa gaa aac gtt gat gcc ggt 384

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly	
115 120 125	
gaa cgt gca aaa cag gct cta gcg ttc gaa cgc act gat ttc gac cag	432
Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln	
130 135 140	
gtt cgt tca ctc atg gaa aat agc gat cgc tgc cag gat ata cgt aat	480
Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn	
145 150 155 160	
ctg gca ttt ctg ggg att gct tat aac acc ctg tta cgt ata gcc gaa	528
Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu	
165 170 175	
att gcc agg atc agg gtt aaa gat atc tca cgt act gac ggt ggg aga	576
Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg	
180 185 190	
atg tta atc cat att ggc aga acg aaa acg ctg gtt agc acc gca ggt	624
Met Leu Ile His Ile Gly Arg Thr Lys Thr Leu Val Ser Thr Ala Gly	
195 200 205	
gta gag aag gca ctt agc ctg ggg gta act aaa ctg gtc gag cga tgg	672
Val Glu Lys Ala Leu Ser Leu Gly Val Thr Lys Leu Val Glu Arg Trp	
210 215 220	
att tcc gtc tct ggt gta gct gat gat ccg aat aac tac ctg ttt tgc	720
Ile Ser Val Ser Gly Val Ala Asp Asp Pro Asn Asn Tyr Leu Phe Cys	
225 230 235 240	
cgg gtc aga aaa aat ggt gtt gcc gcg cca tct gcc acc agc cag cta	768
Arg Val Arg Lys Asn Gly Val Ala Ala Pro Ser Ala Thr Ser Gln Leu	
245 250 255	
tca act cgc gcc ctg gaa ggg att ttt gaa gca act cat cga ttg att	816
Ser Thr Arg Ala Leu Glu Gly Ile Phe Glu Ala Thr His Arg Leu Ile	
260 265 270	
tac ggc gct aag gat gac tct ggt cag aga tac ctg gcc tgg tct gga	864
Tyr Gly Ala Lys Asp Asp Ser Gly Gln Arg Tyr Leu Ala Trp Ser Gly	
275 280 285	
cac agt gcc cgt gtc gga gcc gcg cga gat atg gcc cgc gct gga gtt	912
His Ser Ala Arg Val Gly Ala Ala Arg Asp Met Ala Arg Ala Gly Val	
290 295 300	
tca ata ccg gag atc atg caa gct ggt ggc tgg acc aat gta aat att	960
Ser Ile Pro Glu Ile Met Gln Ala Gly Gly Trp Thr Asn Val Asn Ile	
305 310 315 320	
gtc atg aac tat atc cgt aac ctg gat agt gaa aca ggg gca atg gtg	1008
Val Met Asn Tyr Ile Arg Asn Leu Asp Ser Glu Thr Gly Ala Met Val	
325 330 335	
cgc ctg ctg gaa gat ggc gat ctc gag cca tct gct gga gac atg aga	1056
Arg Leu Leu Glu Asp Gly Asp Leu Glu Pro Ser Ala Gly Asp Met Arg	
340 345 350	
gct gcc aac ctt tgg cca agc ccg ctc atg atc aaa cgc tct aag aag	1104
Ala Ala Asn Leu Trp Pro Ser Pro Leu Met Ile Lys Arg Ser Lys Lys	

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 018/023
 17
 432
 480
 528
 576
 624
 672
 720
 768
 816
 864
 912
 960
 1008
 1056
 1104

355	360	365	
aac agc ctg gcc ttg tcc ctg acg gcc gac cag atg gtc agt gcc ttg Asn Ser Leu Ala Leu Ser Leu Thr Ala Asp Gln Met Val Ser Ala Leu 370 375 380			1152
ttg gat gct gag ccc ccc ata ctc tat tcc gag tat gat cct acc aga Leu Asp Ala Glu Pro Pro Ile Leu Tyr Ser Glu Tyr Asp Pro Thr Arg 385 390 395 400			1200
ccc ttc agt gaa gct tcc atg atg gcc tta ctg acc aac ctg gca gac Pro Phe Ser Glu Ala Ser Met Met Gly Leu Leu Thr Asn Leu Ala Asp 405 410 415			1248
agg gag ctg gtt cac atg atc aac tgg gcg aag agg gtg cca ggc ttt Arg Glu Leu Val His Met Ile Asn Trp Ala Lys Arg Val Pro Gly Phe 420 425 430			1296
gtg gat ttg acc ctc cat gat cag gtc cac ctt cta gaa tgt gcc tgg Val Asp Leu Thr Leu His Asp Gln Val His Leu Leu Glu Cys Ala Trp 435 440 445			1344
cta gag atc ctg atg att ggt ctc gtc tgg cgc tcc atg gag cac cca Leu Glu Ile Leu Met Ile Gly Leu Val Trp Arg Ser Met Glu His Pro 450 455 460			1392
ggg aag cta ctg ttt gct cct aac ttg ctc ttg gac agg aac cag gga Gly Lys Leu Leu Phe Ala Pro Asn Leu Leu Leu Asp Arg Asn Gln Gly 465 470 475 480			1440
aaa tgt gta gag gcc atg gtg gag atc ttc gac atg ctg ctg gct aca Lys Cys Val Glu Gly Met Val Glu Ile Phe Asp Met Leu Leu Ala Thr 485 490 495			1488
tca tct cgg ttc cgc atg atg aat ctg cag gga gag gag ttt gtg tgc Ser Ser Arg Phe Arg Met Met Asn Leu Gln Gly Glu Glu Phe Val Cys 500 505 510			1536
ctc aaa tct att att ttg ctt aat tct gga gtg tac aca ttt ctg tcc Leu Lys Ser Ile Ile Leu Leu Asn Ser Gly Val Tyr Thr Phe Leu Ser 515 520 525			1584
agc acc ctg aag tct ctg gaa gag aag gac cat atc cac cga gtc ctg Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530 535 540			1632
gac aag atc aca gac act ttg atc cac ctg atg gcc aag gca ggc ctg Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545 550 555 560			1680
acc ctg cag cag cag cac cag cgg ctg gcc cag ctc ctc ctc atc ctc Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565 570 575			1728
tcc cac atc agg cac atg agt aac aaa ggc atg gag cat ctg tac agc Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580 585 590			1776
atg aag tgc aag aac gtg gtg ccc ctc tat gac ctg ctg ctg gag gcg Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Glu Ala 595 600 605			1824

gcg gac gcc cac cgc cta cat gcg ccc act agc cgt gga ggg gca tcc 1872
 Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser
 610 615 620

gtg gag gag acg gac caa agc cac ttg gcc act gcg ggc tct act tca 1920
 Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser
 625 630 635 640

tcg cat tcc ttg caa aag tat tac atc acg ggg gag gca gag ggt ttc 1968
 Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe
 645 650 655

cct gcc aca gct tga 1983
 Pro Ala Thr Ala
 660

<210> 8

<211> 660

<212> PRT

<213> Artificial sequence

<223> Chimeric sequence Homosapiens-Bacteriophage P1

<400> 8

Met Ser Asn Leu Leu Thr Val His Gln Asn Leu Pro Ala Leu Pro Val
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Asp Ala Thr Ser Asp Glu Val Arg Lys Asn Leu Met Asp Met Phe Arg
 20 25 30

Asp Arg Gln Ala Phe Ser Glu His Thr Trp Lys Met Leu Leu Ser Val
 35 40 45

Cys Arg Ser Trp Ala Ala Trp Cys Lys Leu Asn Asn Arg Lys Trp Phe
 50 55 60

Pro Ala Glu Pro Glu Asp Val Arg Asp Tyr Leu Leu Tyr Leu Gln Ala
 65 70 75 80

Arg Gly Leu Ala Val Lys Thr Ile Gln Gln His Leu Gly Gln Leu Asn
 85 90 95

Met Leu His Arg Arg Ser Gly Leu Pro Arg Pro Ser Asp Ser Asn Ala
 100 105 110

Val Ser Leu Val Met Arg Arg Ile Arg Lys Glu Asn Val Asp Ala Gly
 115 120 125

Glu Arg Ala Lys Gln Ala Leu Ala Phe Glu Arg Thr Asp Phe Asp Gln
 130 135 140

Val Arg Ser Leu Met Glu Asn Ser Asp Arg Cys Gln Asp Ile Arg Asn
 145 150 155 160

Leu Ala Phe Leu Gly Ile Ala Tyr Asn Thr Leu Leu Arg Ile Ala Glu
 165 170 175

Ile Ala Arg Ile Arg Val Lys Asp Ile Ser Arg Thr Asp Gly Gly Arg
 180 185 190

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Met	Leu	Ile	His	Ile	Gly	Arg	Thr	Lys	Thr	Leu	Val	Ser	Thr	Ala	Gly	
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Val	Glu	Lys	Ala	Leu	Ser	Leu	Gly	Val	Thr	Lys	Leu	Val	Glu	Arg	Trp	
	210					215					220					
Ile	Ser	Val	Ser	Gly	Val	Ala	Asp	Asp	Pro	Asn	Asn	Tyr	Leu	Phe	Cys	
225					230					235					240	
Arg	Val	Arg	Lys	Asn	Gly	Val	Ala	Ala	Pro	Ser	Ala	Thr	Ser	Gln	Leu	
			245						250					255		
Ser	Thr	Arg	Ala	Leu	Glu	Gly	Ile	Phe	Glu	Ala	Thr	His	Arg	Leu	Ile	
		260						265					270			
Tyr	Gly	Ala	Lys	Asp	Asp	Ser	Gly	Gln	Arg	Tyr	Leu	Ala	Trp	Ser	Gly	
	275						280					285				
His	Ser	Ala	Arg	Val	Gly	Ala	Ala	Arg	Asp	Met	Ala	Arg	Ala	Gly	Val	
	290					295					300					
Ser	Ile	Pro	Glu	Ile	Met	Gln	Ala	Gly	Gly	Trp	Thr	Asn	Val	Asn	Ile	
305					310					315					320	
Val	Met	Asn	Tyr	Ile	Arg	Asn	Leu	Asp	Ser	Glu	Thr	Gly	Ala	Met	Val	
			325						330					335		
Arg	Leu	Leu	Glu	Asp	Gly	Asp	Leu	Glu	Pro	Ser	Ala	Gly	Asp	Met	Arg	
			340					345					350			
Ala	Ala	Asn	Leu	Trp	Pro	Ser	Pro	Leu	Met	Ile	Lys	Arg	Ser	Lys	Lys	
		355					360					365				
Asn	Ser	Leu	Ala	Leu	Ser	Leu	Thr	Ala	Asp	Gln	Met	Val	Ser	Ala	Leu	
	370					375					380					
Leu	Asp	Ala	Glu	Pro	Pro	Ile	Leu	Tyr	Ser	Glu	Tyr	Asp	Pro	Thr	Arg	
385					390					395					400	
Pro	Phe	Ser	Glu	Ala	Ser	Met	Met	Gly	Leu	Leu	Thr	Asn	Leu	Ala	Asp	
			405						410					415		
Arg	Glu	Leu	Val	His	Met	Ile	Asn	Trp	Ala	Lys	Arg	Val	Pro	Gly	Phe	
		420						425					430			
Val	Asp	Leu	Thr	Leu	His	Asp	Gln	Val	His	Leu	Leu	Glu	Cys	Ala	Trp	
	435						440					445				
Leu	Glu	Ile	Leu	Met	Ile	Gly	Leu	Val	Trp	Arg	Ser	Met	Glu	His	Pro	
	450					455					460					
Gly	Lys	Leu	Leu	Phe	Ala	Pro	Asn	Leu	Leu	Leu	Asp	Arg	Asn	Gln	Gly	
465					470					475					480	
Lys	Cys	Val	Glu	Gly	Met	Val	Glu	Ile	Phe	Asp	Met	Leu	Leu	Ala	Thr	
			485						490					495		
Ser	Ser	Arg	Phe	Arg	Met	Met	Asn	Leu	Gln	Gly	Glu	Glu	Phe	Val	Cys	
		500						505					510			
Leu	Lys	Ser	Ile	Ile	Leu	Leu										

21

515	520	525
Ser Thr Leu Lys Ser Leu Glu Glu Lys Asp His Ile His Arg Val Leu 530	535	540
Asp Lys Ile Thr Asp Thr Leu Ile His Leu Met Ala Lys Ala Gly Leu 545	550	555 560
Thr Leu Gln Gln Gln His Gln Arg Leu Ala Gln Leu Leu Leu Ile Leu 565	570	575
Ser His Ile Arg His Met Ser Asn Lys Gly Met Glu His Leu Tyr Ser 580	585	590
Met Lys Cys Lys Asn Val Val Pro Leu Tyr Asp Leu Leu Leu Glu Ala 595	600	605
Ala Asp Ala His Arg Leu His Ala Pro Thr Ser Arg Gly Gly Ala Ser 610	615	620
Val Glu Glu Thr Asp Gln Ser His Leu Ala Thr Ala Gly Ser Thr Ser 625	630	635 640
Ser His Ser Leu Gln Lys Tyr Tyr Ile Thr Gly Glu Ala Glu Gly Phe 645	650	655
Pro Ala Thr Ala 660		

<210> 9
 <211> 20
 <212> DNA
 <213> Homo sapiens

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20

<210> 10
 <211> 20
 <212> DNA
 <213> Homo sapiens

<400> 10
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20

<210> 11
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 11
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21

<210> 12
 <211> 20
 <212> DNA

